

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

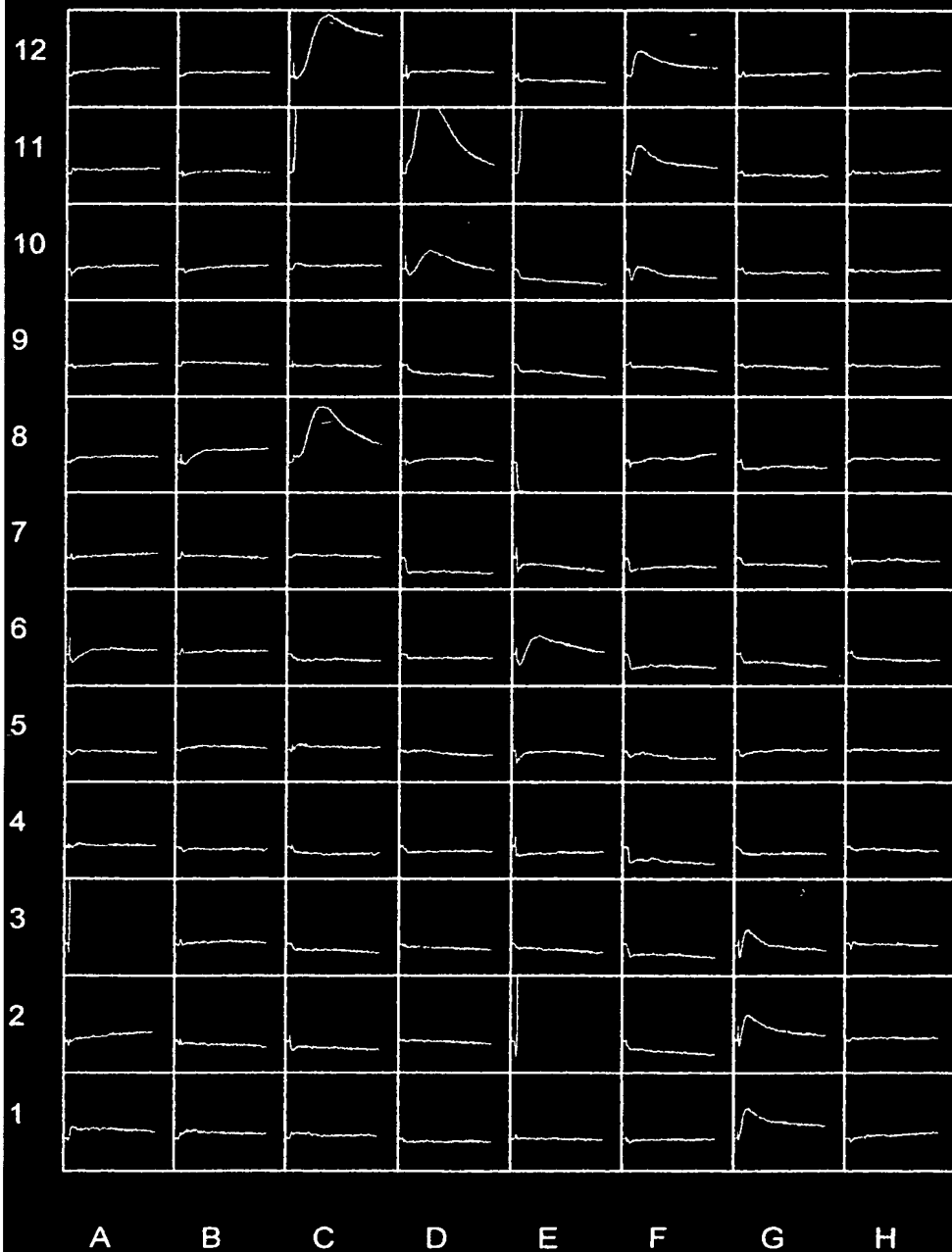
Figure 2

061500_n7.fid

HEC293 Parental

22.2

15106180.



Range = (-1000 , 2000)

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

Figure 3

CLUSTAL W (1.74) multiple sequence alignment

```

NTR1_RAT      MHLNSSVPQGTGPEPDAQPFSGPQSEMEATFLALSLSNGSGNTSESDTAGPNSDLDVNTD
PFI-002      -----MEKLQNASWIYQQKLEDPFQKH-----LNSTEEYLAFLCGPRRS---
               *   .   *   .   *   .   *   .   *   .   *   .

NTR1_RAT      IYSKVLVTAIYLALFVVGTGNSVTAFTLARKKSLQSLQSTVHYHLGSLALSDDLILLLA
PFI-002      HF-FLPVSVVYVPIFVVGVIGNVLVCLVILQ---HQAMKTPTNYLFSLAVSDLLVLLLG
               :   :   *   .   .   .   .   .   .   .   .   .   .   .   .   .   .
               :   :   *   .   .   .   .   .   .   .   .   .   .   .   .   .

NTR1_RAT      MPVELYNFIWVHHPWAFGDAGCRGYYFLRDACTYATALNVASLSVERYLAICHFPKAKTL
PFI-002      MPLEVY-EMWRNYPFLFGPVGCYFKTALFETVCFASILSITTVSVRYVAILHPFRAKLQ
               *   .   .   .   .   .   .   .   .   .   .   .   .   .   .   .
               :   :   *   .   .   .   .   .   .   .   .   .   .   .   .   .

NTR1_RAT      MSRSRTKKFISAIWLASALLAIPMLFTMGLQN-RSGDG-THPGGLVCTPIVDTATVKVVI
PFI-002      STRRRALRILGIVWGFSVLFSLPNTSIHGKIFHYFPNGSLVPGSATCTVIKPMWIYNFII
               :   *   :   .   .   .   .   .   .   .   .   .   .   .   .   .
               :   *   :   .   .   .   .   .   .   .   .   .   .   .   .   .

NTR1_RAT      QVNTFMSFLFPMLVISILNTVIANKLTVMVHQAAEQGRVCTVGTHNGLEHSTFNMTIEPG
PFI-002      QVTSFLFYLLPMTVISVLYYLMALR-----
               *   .   .   .   .   .   .   .   .   .   .   .   .   .   .

NTR1_RAT      RVQALRHGVLVLRVVI AFVVCWLPYHVRRMLFCYISDEQWTTFLFDYHYFYMLTNALF
PFI-002      -----

NTR1_RAT      YVSSAINPILYNLVSANFRQVFLSTLACLCPGWRHRRKKRPTFSRKPNMSSNHAFSTSA
PFI-002      -----

NTR1_RAT      TRETLY
PFI-002      -----

```


APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

Figure 5

Figure 5A

Nucleotide sequence coding for PFI-002

SEQ ID NO: 1

ATGGAAAACTTCAGAATGCTTCCTGGATCTACCAGCAGAACTAGAAGATC
CATTCCAGAAACACCTGAACAGCACCGAGGAGTATCTGGCCTTCCTCTGCGG
ACCTCGGCGCAGCCACTTCTTCCTCCCCGTGTCTGTGGTGTATGTGCCAATTTT
TGTGGTGGGGGTCATTGGCAATGTCCTGGTGTGCCTGGTGATTCTGCAGCACC
AGGCTATGAAGACGCCACCACTACTACCTCTTCAGCCTGGCGGTCTCTGA
CCTCCTGGTCCTGCTCCTTGGAATGCCCTGGAGGTCTATGAGATGTGGCGCA
ACTACCCTTTCTTGTTTCGGGCCCCGTGGGCTGCTACTTCAAGACGGCCCTCTTT
GAGACCGTGTGCTTCGCCTCCATCCTCAGCATCACCACCGTCAGCGTGGAGC
GCTACGTGGCCATCCTACACCCGTTCCGCGCCAACTGCAGAGCACCCGGCG
CCGGGCCCTCAGGATCCTCGGCATCGTCTGGGGCTTCTCCGTGCTCTTCTCCC
TGCCCAACACCAGCATCCATGGCATCAAGTTCCACTACTTCCCCAATGGGTCC
CTGGTCCCAGGTTTCGGCCACCTGTACGGTCATCAAGCCCATGTGGATCTACA
ATTCATCATCCAGGTCACCTCCTTCTATTCTACCTCCTCCCCATGACTGTCA
TCAGTGTCTCTACTACCTCATGGCACTCAGAGTGAGTATCTAG

Figure 5B

Amino acid sequence coding for PFI-002

SEQ ID NO: 2

MEKLQNASWIYQQKLEDPFQKHLNSTEEYLAFLCGPRRSHFFLPVSVVYVPIFVV
GVIGNVLVCLVILQHQAMKTPTNYLFLSLAVSDLLVLLLGMPLEVYEMWRNYPF
LFGPVGCYFKTALFETVCFASILSITTVSVERYVAILHPFRAKLQSTRRRALRILGI
VWGFSVLFSLPNTSIHGKIFHYFPNGSLVPGSATCTVIKPMWIYNFIIQVTSFLFYL
LPMTVISVLYYLMALRVSI

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

Figure 6

SEQ ID NO: 3
ACCATGGCAGGGATGGAAAACTT

SEQ ID NO: 4
GCTCTGAAAGAATTCAGGTTTTG

SEQ ID NO: 5
TCCAGAAACACCTGAACAGC

SEQ ID NO: 6
GAGGTAGAATAGGAAGGAGG

0564725-100000